

Figure 1

MAPK Targets Include Proteins Known or Predicted to Enter the Secretory Pathway

1 secreted endopolygalacturonase

GPI-linked cell surface adhesion factor FL011

TOT10/YEL033W novel

SRD1 Zinc finger protein

TOT12/YKR105C putative permease

TOT13/YOR225W putative membrane protein

GPI-linked cell surface adhesion factor FL05

DDR48 cell surface protein

TOT11/YLR042C GPI-linked cell surface protein

Homolog of mating morphogenesis protein Afr1 TOT7/YER158C

Homolog of Chitin Synthase III subunit TOT8/YIL117C

TOT20/YHL049C telomeric protein family member

TOT15/ YLR434C novel

TOT14/YBR113W putative membrane protein

TOT9/YIR013C Zinc finger protein

phosphate transporter, sugar permease family PH084

protein mannosyltransferase homolog KTR2

Sac1-related inositol phosphate 5-phosphatase homolog

Sytematic Knockout Experiments

GENE	Haploid Invasion	Diploid Filamentation
PGU1	+++	+++
FLO11	-	-
TOT10/YEL033W	+	+
SRD1	ND	ND
TOT12/YKR105C	+++	+++
TOT13/YOR225W	+++	+++
FLO5	+++	++++
DDR48	+++	+++
TOT11/YLR042C	+++	+++
TOT7/YER158C	+++	+++
TOT8/YIL117C	+++	+++
TOT20/YHL049C	ND	ND
TOT15YLR434C	+++	+++
TOT14/YBR113W	+++	+++
TOT9/YIR013C	+++	+++
PHO84	+++	+++
KTR2	+++	+++
SJH1	+++	+++

Filamentation MAPK Pathway Controls Pectinolysis via PGU mull phenotypes B

Figure 4

Gene Induction by the Plant-Specific Carbohydrate Polygalacturonic Acid and Its Hydrolysis Product

Genes Selectively Induced by Polygalacturonic Acid

dene	gĄ.	PGA/-	Protein Information
XBP1	2.40	6.65	Stress-induced transcriptional repressor
YHR217C(f)	1.30	9.00	Protein of unknown function
YPL080C	2.80	5.70	Protein of unknown function
YPR098C	1.16	5.49	Protein of unknown function
YHL040C	2.04	2.00	Putative MFS Permease
XOL080C	1.35	4.74	Protein with similarity to Rnh70p and Pan2p
PH084	1.39	4.70	phosphate transport, sugar permease homolog*
YMR293C	1.29	4.07	Protein with similarity to amidase
YLR184W	1.33	3.24	Protein of unknown function
YIL011W	1.01	3.01	Protein with similarity to PAU1 family
CYT1	1.02	2.83	Cytochrome c1
ATP11	1.29	2.65	F1-ATP synthase assembly protein
YOR091W	1.17	2.51	Protein of unknown function
PAU3	1.02	2.46	Stress-induced protein of the PAU1 family
SK01	0.47	2.35	ATF/CREB transcriptional repressor
MSI4	0.73	5.06	Rab guanine nucleotide dissociation inhibitor
	Regula	ted by Fi	Regulated by Filamentation MAPK Pathway*

Genes Selectively Induced by Galacturonic Acid

Protein Information	Vacuolar sorting protein, dynamin GTPase
PGA/-	1.69
GA/-	4.03
gene	VPS1

Gene Repression by the Plant-Specific Carbohydrate Polygalacturonic Acid and its Hydrolysis Product

Genes Selectively Repressed by Polygalacturonic Acid

lene	GA.	PGA-	Protein Information
COP1/SEC33	0.63	0.17	alpha subunit of coatamer complex
/OL002C	1.36	0.18	Protein of unknown function
/DL173W	96.0	0.24	Protein of unknown function
,002	1.37	0.25	coenzyme ((ubianinone) biosynthesis
7L176C (f)	0.86	0.30	Protein with similarity to PAII1 family
/FL032W	0.80	0.30	Protein of unknown function
37 PS33A	1.10	0.34	Ribosomal protein S28A
1 <i>RC35</i>	1.25	0.39	Component of ARP2/3 complex
3PS26A	0.87	0.39	Ribosomal protein S26A
PS10A	1.02	1.02 0.46	Ribosomal protein S10A

Genes Selectively Repressed by Galacturonic Acid

A/- Protein Information			Spindle pole body duplication factor	
PG	0	1.46	1.02	2.35
GA/-	0.12 0.38	0.24	0.29	0.47
gene	YEL033W	VID24	NDC1	SK01

*Regulated by the Filamentation MAPK Pathway

					TO BEING				
floor=20	date are sorted as TEC1-high copy/tec1	ed as TEC	1-high copy/	actá: Ivi ele	na have been	Detroed	Colonial Angle Colonial	-	1
mex-min>90			_						
sceling-bulk		1	-						
Sene	¥	5	ste 12	107	TCHC	STEILA	4) 14) (dax		
STAT (YHO19C)	262	•	4.7	9	173 748	2020	(5) Lett 133 t be all n		
COLUMN TO THE PARTY OF THE PART	9		20	34	21 269	20			
CODE COLOR POR	8/1			1	30	0.0	uci (Stift) "andymon" (Stid (Stift)		
ODE N DOOD			1		0071		SLOSE DIACED, Universit, Universit, University, Univer		-
SBOTOS			200		200	000	10 S 20 S 1 TO S 10 S 1		-
GRE YAPOOBC (P	657	:	1		336	1250	FOR A STATE OF THE	-	
ORF YHROIGE Brown 1 (0)	261	!			74	772	CANADA CONTRACTOR CONT		
OBE YKBIOK				1			1. (1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1		
ORF YORZSW					100				
OBF VI BANC	,	, ,	:_		200		(1.1.2.1.1.1.1.1.1.1.1.1.1.1.1.1.1.1.1.1		
OBE VBB113W					200		112 ZHUKUM HOKKOM HOKKOM	-	
ODE ANDOOR		•		-	200	100	10.72 & 10.12 Medican, 110.22 Medican and 10.72		
Operation of the control of the cont					200		11/1/4 i T. 11 10 1/1/1/1 (T. 11 1/1/1 1/1 1/1 1/1 1/1 1/1 1/1 1/1 1		
200					0.5		Profess of universe profess		
PHO64 [TML 123C]		;	1		26 114	7.7	Right (Linky Anglang), physophato/Be, pymyskter, newber of angle, respector (seeky		
OH TAKONC LL	124	=	:	348	620 702	2168	Fr. 3. th. u. f. unbrich.		
KING [INHOBIN)			30	2	20 158		Rander Hannifalan (alabe el 1962 Larla, lavolved la Malinked alacevy laila		
OPE WAR 173W	50	;	33	20	20 136	•	Biggs process induced by hear, aboch, clid, disease, or operating the second control of the disease, or operating the second control of the disease, or operating the second control of the disease of th		
TEC1 (YBROB3W)	612	ń	332	4.5	62 501	223	. 828 Tames tim soul artives or involved with state in use while he is not seen from		
DAM! (YJR150C)	021	;	29	20	108	20	20 ft. i ein indesed during annerelbie steweb		
SOR! (YJR159W) (_n)	132	•	50	-	163 - 233	208	Satistical detained regerence Lengthics, and MAR to Lengther and MAR (1991) and 1992		
ORF YILLI7C	50	:	20	20	20 69	195	States of underweit function		
ORF YHR214C-8 exon 2 Lft	305	=	137	197	62 472	267	Presidental untransfer function		
ORF YNLZS6W	8.9			67	55 117	9	60 Protein with similarity to betretial diludirants aventuas		
GAP (YKRO39W)	101	. =	26	3	424	404	for a facility of the control of the	of the same	1200
ORF YFLICTOW		:	_		47		WORLD TO SERVICE AND		12.
OBE VI BISOC		,							
ODE VOI DEBAN		, .	:	1			1.12.11.12.11.12.12.12.12.12.12.12.12.12		-
The second					77	2	20 Feelen with a military of Cyandybia paradoxa, the accel profession from		
COLUMN TIPLE					20	-	31 (throthe) That Me water, with piel 12 (for the and Greit)		-
Out of the state o	•	!	-			2	27.44.0. 41.0. e.m. 41.55 c.m. 92.540. Rve 16.70. Attrip. end State		
PHOTO LINE COM	7	•			27		12.0 cm, 19.1 and 92. absorbed in advances a second at 50. ember of the Pt. Central properties and 19 lated to IPSA absorbed asses.		
GCT1 TOT SOW)	•	,	;	:	24		SPACE OF CORPUSED POSE IN A CORPUSED TO SEASON OF THE PROPERTY		
HHAT IT BLUBSON	20		:	23	151		Mone and to come a comparate in all advices has tign, Memorous in mental and the contract of t		
CHE THEORY CO	50		20	20	20 \$7		train with time latery to other min elementable transfert matering including Friles. and Villa in. codes from a sustaines for 1 marks.		
MONTH INTO		7, 1	;	:	20		Fig. 11 bits mith with a first grid of the second		
MUP! (YGHOSSW)	- 10	- ;	;	;	280 257	192	And the state of t		
OF TARGE	1042	3	900	700	1821 1231	1531	State State in the state of the state of the bloom the bloom is as in first trying then		
OF TOTAL	253	•		†	40		Erickin with eini bulky to viening, we house energy of the Company		
TOTAL (YOR 161W)	401			i	133	0.1	Grand that, interested with protein phospheters, XC		
PDE2 (YORGOC)	102			-	96	120	E. A. Engelskeing der de		
CWP1 (YKLO96W)	•	_		176	186	430	81002012610.01.19.cg1] ### 12.01.10.10.10.10.10.10.10.10.10.10.10.10.		
ORF YOU ISSUE	67	.,		06	121	-	Postario sich einstatus de Presdenne, so. in alba), sulfacen		
ORF YARDEEW LD	86	•		36	40 205	101	Profesional uniquement and threater good for identical proteins		
AIP2 (YDL178W)	209	_		217	35 197	128	Antib interact has receiped of Distant development bidin		
ORF YGROSTC				176	20		The second secon		-
RFC3 (YNL290W)	*	•		20	20 105		Participation Country Country and the farm has trained and the country of the country and the country of the co		:
OFF YEROKOW	255	Ξ		78	25 236		1 to the first is an included a second and the first is a second and t		
TIP (YBROATC)	2232	1574		150	182 3483		CAM Matter inhancement and the call of the		
OBE VI BOXIC	,						100 CONT. 100 CO		
DC: CVN: 200MD	1	,					THE THE THE WAY OF THE TOTAL THE TRANSPORT OF THE TRANSPO	-	
400.000			,				\$1.00 LEGS (10.00 - Con., 10.00 St C.1.0 COS. 200 - C. Legs		
COLUMN TO THE PARTY OF THE PART		,	•				CONTINUATION OF THE CONTINUE O	-	
Car Totales	199		:	-	35		940 Historia of unthrow (unstrion		
FINI (VEH14SC)	239	2	!	!	230 415	383	309 Jim Faltense that mediate high effinity from unake		
CH TANDISM	1947	ě	ŧ	1	1769	2619	Pretrie of unhane lungion		
CIT2 (YCROSC)	1555	•	:	1815	1324	1662	CHIEVE STADERS. DESCRIBEDE L'ESTABLE SINGED STALING L'AND STALING STALING STADES SE		
OHF YORKSC	9	•	:	59	135	2	State of mark on Gravitan		
OHE YELDORW	50	•			127	43	Institution with aire in 1912 as Ascip. Pri Sp. Ascip. Pri Sp. and sther worders of the river live in the live in the contract of the contract		
SVSI (YPL163C)	650	÷	;	1	74 858		Spilos, and the spines rish protein goviles for who have		
ECO1 (74,196C)	292	ě	:	;	695 1216		THE AMERICAN PERSON IN SOME IS A SOME SET AND A SOM	-	-
OH! YJI 165W	165	-	:	1	340	337	Operation of authors and an arministration of the contract of		
OFF YHRIOSW	9			-	40		France Claud Con Lugaria		
VID24 (YBB 105C)	127	•	63	-	115 126		Productional Society in incident and deposit of their statement of the sta		
OF YORSEW	9	.,	•	_	22 76	9	P. 3 Fin C. Milhard (1914) (20		
LSC2 (YGP244C)	67.	•		.	60	560	Bet all and benefits of Leuce hard and examines used developed by London and Benefit.	-	-
C(P1 (YORZ50C)	2			7	31	142	satists of characters and collected of active In accorded for Present an engine of signifials		

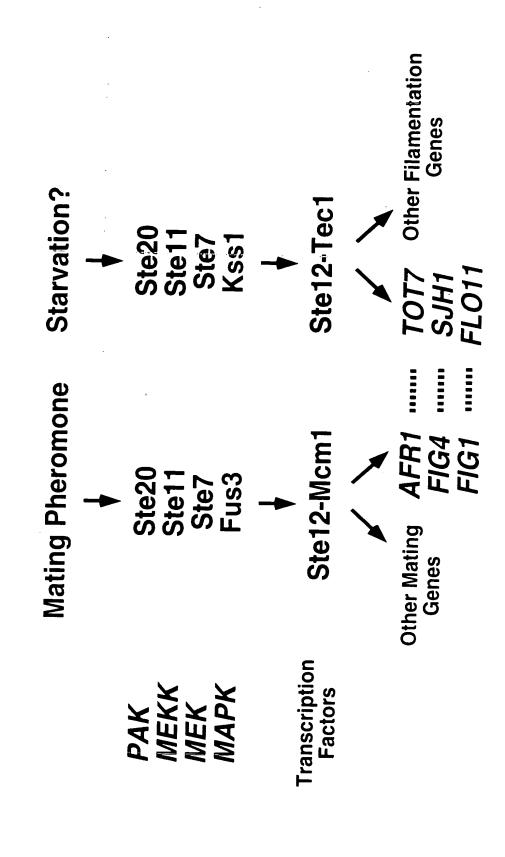


NAME=GA	T	i	-	1	·
gene	YPD	GA	PGA	GAYPD	PGAYPD
ORF YIL101C	20				
ORF YLR344W exon 1 (_i)	33				
ORF YHR217C (_r_i)	20				
ORF YHR217C (_f)	20				6.00
ORF YPL080C	20				
ORF YPR098C	37				5.49
ORF YHL040C	27				
ORF YOL080C	23				5.00 4.74
PHO84 (YML123C)	33				
ORF YMR293C	28				
ORF YLR184W	66				
ORF YIL011W	153				
ORF YJR027W exon 2 (_f)	156				
CYT1 (YOR065W)	91				
ORF YLL025W (_f)	251				
ORF YML039W exon 2 (_f)	192				2.76
ATP11 (YNL315C)	51				2.73
ORF YOR091W	59		 		2.65
ORF YMR143W exon 1 (_i)	385				2.51
ORF YJR029W exon 2 (_i)	71				2.50 2.46
PAU3 (YCR104W) (_f)	180	184			
SKO1 (YNL167C)	43	20			2.46
PRE3 (YJL001W) exon 1	112	166			2.35
ORF YMR045C exon 2 (_f)	93	132			2.15
ORF YNL006W	77	100	·	·	2.12
MSI4 (YOR370C)	63	46	·		2.09
ORF YPR139C	91	122		 	2.06
SPO15 (YKR001C)	35	141			2.05
HHO1 (YPL127C)	81	45			1.69
ILV3 (YJR016C)	119	72			1.67
ORF YBR105C	82	20		,	1.53
LYS4 (YDR234W)	479	244			1.46
ORF YOR009W	144	310	158		1.20
NDC1 (YML031W)	113	33			1.10
ORF YOL073C	143	180			1.02
ORF YJL223C (_f)	134	175	81		0.62
ORF YMR242C	1170	1227			0.60
ORF YOR248W (_f)	497	422	239	 	0.52
ORF YPL081W exon 1	159	135	75		0.48
ORF YML019W	177	91	82		0.47
ORF YOR293W exon 1 (_f)	3170	3237			0.46
ORF YMR050C exon 1 (_f)	374		1446		0.46
RPS26A (YGL189C)	11511				0.45
ORF YNR035C	200	9978 249	4526	·	0.39
ORF YEL033W	172	20			0.39
TSL1 (YML100W)	103	20			0.38
RPS33A (YOR167C) (_f)	1726	1899	39		0.38
ORF YFL032W	122	98	589	·	0.34
ORF YIL176C (_f)	115	99	37		0.30
COQ2 (YNR041C)	84		34 21		0.30
ORF YDL173W	141	115 136			0.25
ORF YOL002C	111	151	34		0.24
ORF YDL145C	118	74	20		0.18
PROCESS=scaling			20	0.63	0.17
PROCESS=scaling	METHOD=bulk S GENES=6365				
PROCESS=assemble.pl			MANY	DATO	
	GEIVES=33	DIFF=80	MAX=	RAT=2	
=	<u> </u>				

GA.filt.GAsort

NAME=GA	1	T			
gene	YPD	GA	PGA	GAYPD	PGAYPD
ORF YLR344W exon 1 (_i)	33	138	208	3! 4.18	··
SPO15 (YKR001C)	35	141	59		
ORF YPL080C	20	 	114		
ORF YML039W exon 2 (_f)	192	 			2.73
ORF YIL101C	20				6.65
ORF YMR143W exon 1 (_i)	385	·			2.50
ORF YJR027W exon 2 (_f)	156	·			2.94
ORF YOR009W	144				
ORF YHL040C	27				
PRE3 (YJL001W) exon 1	112				
ORF YHR217C (_r_i) ORF YMR045C exon 2 (_f)	20	•			
ORF YLL025W (_f)	93 251	 			
PHO84 (YML123C)	33				
COQ2 (YNR041C)	84				
ORF YOL002C	111	,			
ORF YOL080C	23				
ORF YPR139C	31				
ORF YJR029W exon 2 (_f)	71				
ORF YLR184W	66	 			
ORF YJL223C (_f)	134				
ORF YHR217C (_f)	20	:			
ORF YNL006W	77				
ATP11 (YNL315C)	51	66			
ORF YMR293C	28	36			
ORF YOL073C	143	180			
ORF YNR035C	200		78		0.39
ORF YOR091W	59	69		1.17	
ORF YPR098C	37	43			
RPS33A (YOR167C) (_f)	1726	1899			
ORF YMR242C	1170				0.52
PAU3 (YCR104W) (_f)	180				2.46
CYT1 (YOR065W)	91	93	257		
ORF YOR293W exon 1 (_f)	3170	3237	1446		0.46
ORF YIL011W	153	154			3.01
ORF YDL173W RPS26A (YGL189C)	141	136			0.24
ORF YIL176C (_f)	11511	9978	4526		0.39
ORF YOR248W (_f)	497	99 422	34		0.30
ORF YPL081W exon 1	159	135	239 75		0.48
ORF YFL032W	122	98	37		0.47
MSI4 (YOR370C)	63	46			2.06
ORF YMR050C exon 1 (_f)	374	263	169		0.45
ORF YDL145C	118	74	20		0.45
ILV3 (YJR016C)	119	72	182		1.53
HHO1 (YPL127C)	81	45	135		1.67
ORF YML019W	177	91	82		0.46
LYS4 (YDR234W)	479	244	576		1.20
SKO1 (YNL167C)	43	20	101		2.35
NDC1 (YML031W)	113	33	115		1.02
ORF YBR105C	82	20	120		1.46
TSL1 (YML100W)	103	20	39	0.19	0.38
ORF YEL033W	172	20	66	0.12	0.38
	METHOD=bulk S				
PROCESS=assemble.pl	GENES=6365				
	GENES=53	DIFF=80	MAX=	RAT=2	
=					

Homologous Genes Induced by Filamentation and Mating MAPK Pathways



	Į.	196	Ste	ste12	ste7	2	STE11-4	YPD Title Lines
MFA1 (YDR461W)	3803	(2)	5138	20	28	3378		2.262 Mains preconnece a factor, exported from cell by Steep
ANB1 (YJR047C)	1285	2	1668	31	110	1090		Translation initiation factor ell'5A, contains exemisal byjusine modification
HIS3 (YOR202W)	334	4	317	34	09	378	73	
MFA2 (YNL145W)	7879	6	6017	821	1993	3 4780		4674 Maing pheromone a-factor, exported from cell by Stede
STE2 (YFL026W)	998	9	1169	121	178	8 802		598 Ръстовние аръа-Тактог госерия, вечен-втаките пътата съставни примен
ORF YDL 120W	118	80	102	20	4	117		59 Minechoodrial protein involved in respiratory function and trop homeostasis, homolog of human frauexin which is defective in Friedreich's anaxia
ORF YIL121W	286	9	169	52	119	9 212	2	258 Member of major facilitator superfamily (MFS) multidatog -resistance (MIS-MDR) protein family
ORF YOLDZEC	108	8	140	20	2	127		83 Protein of unknown function
ORF YKL120W	906	9	714	168	217	7 741		989 Protein with similarity to members of the mitor-bondrial servic (MCT) family
COS6 (YGR295C)	638	8	480	122	131	1 415		Ç,
CHS2 (YBR038W)	104	7	7.6	20	20	0 60		60 (Thitin symbase II, responsible for primary septum disk
ORF YLR437C	103	3	48	20		0 58		34 Protein of unknown function
ORI2 (YDL105W)	102	2	48	21				20 Protein of unknown function
GPA1 (YHR005C)	168	8	124	37		1 75		39 Citamine nucleokide-binding protein alpha subunit of the pheromone response pathway
ORF YKL137W	117	7	29	27	30	0 67		55 Protein of unknown function
AGA2 (YGL032C)	299	6	538	69		342	18	990 ja - Asgibujania binding subumi
ORF YHR214W (LI)	107	7	64	25	25	5 104		114 Prugin of unknown function (YAR0860W and YHR2141V code for identical pructins)
EU1 (YGL009C)	2205	S	1865	519	489	1758	6	3-bopropylmalate dehydratase, second step in leucine blesynthesis pathway
PDR12 (YPL058C)	198	8	172	47	62	2 115		134 Procein with similarity to Put/26 and Snq20, member of the ATP binding cascute (ABC) superfamily
FAR1 (YJL157C)	258	80	244	85	52	151		35.7 Inhibitar of CA:289-Chilp and CA:289-Chilp binase complexes involved in cell cyrte arrest for mating
WEP2 (YNL142W)	156	9	115	9		3 227		12.3 Annovia permease of low capacity and high affinity
LV3 (YJR016C)	979	6	785	256		1012		1158 Dihydrosyacial debydratase (DAD), third seep in valine, and isodeuxine biraynthesis pathway
VOP4 (YPL043W)	114	4	96	30	29	107		28 Nuckoular projetin required for riboxome biogenesis, has 3 canonical RNA recognition (RRM) domains and one degenerate RNA recognition (RRM) domain
ADE5,7" (YGL234W)	511	_	313	137	114	4 467	-	07 Phosphoribosylamine glycine Bigase (GARSase) + Phosphoribosylformylglycinamidine cyclo-figase (AIRSase), bilunctional person
ORF YMR304C-A	7.	2	98	20	20	107		
MSB2 (YGR014W)	7.1	-	59	20	20	0 110		2.7 Protein for which overproduction suppresses bad emergence defect of cak.24 mutant
MPT5 (YGL178W) exon 1	129	O	89	37	20	71		45 Protein required for high temperature growth, receivery from alpha-factor arres, and mornial lifespain of yeast cells.
WCS2 (YNL283C)	251	-	190	72	125	5 257	2	200 Provein required for maintenence of cell wall integrity and for the arreas response.
RPS24B (YLR367W) exon 1	617	7	747	186	277	7 651		632 Ribosomal protein S22B (1924) (1930) (1932) (1932) (1932) (1932) (1932) (1932) (1932) (1932) (1932) (1932)
STE6 (YKL209C)	143	9	143	44	4	134		302] Membrane transparter of ATP-binding cassette (ABC) hyperfamily responsible for expart of "a" factor mound
BAR1 (YIL015W)	148	80	165	46	7	120		529 Secreted propin-title processe that degrades alpha-facto, (terriporpoid)
CHA1 (YCL064C)	7	7	124	24		1 78		20 11-scripcol attraction describing as (catabulic 1-scripcol) abroading dehydratase)
ORF YER150W	678	æ	374	217	221	1 452	9	623 Process with similarity to Sed ID.
ORF YMR306C	1667	7	1494	541	ļ	1425	1049	0.4.9 Procin with similarity to Bully and other glowans (1.10.7.49212)
ORF YPR156C	340	0	152	112	=	115		233 Member of Ingiar facilities a superfamily (Mi-S) multisting resistance (Mi-S-MI)R) program family
ET4 (YMR319C)	245	5	310	81	7	324	1	159 Law attinity Fell) transport protein
MEP3 (YPR138C)	168	80	107	56	9	7		129 Ammunia pemezas of bish capasity and live addeds
ORF YBR214W	117	7	94	39	4	3 126		41 Proucin with similarity to much proucin of S. pounde
ORF YGRISIC (.)	398	80	421	134	13	0 487		146 Protein of unknown function
FUS3 (YBL016W)	248	80	176	84	9	318		Serine/Observative protein kituses of the MAP kinase family required for cell cycle arrest and for cell flusion during mating
ORF YORZOW	347	7	349	119	13	1 384		292 Protein of unknown function